Title MeSH Enrichment and Semantic analyses

Version 1.28.0

Description MeSH (Medical Subject Headings) is the NLM controlled vocabulary used to manually index articles for MEDLINE/PubMed. MeSH terms were associated by Entrez Gene ID by three methods, gendoo, gene2pubmed and RBBH. This association is fundamental for enrichment and semantic analyses. meshes supports enrichment analysis (over-representation and gene set enrichment analysis) of gene list or whole expression profile. The semantic comparisons of MeSH terms provide quantitative ways to compute similarities between genes and gene groups. meshes implemented five methods proposed by Resnik, Schlicker, Jiang, Lin and Wang respectively and supports more than 70 species.

Depends R (>= 4.1.0)

Imports AnnotationDbi, DOSE, enrichplot, GOSemSim, methods, utils, AnnotationHub, MeSHDbi, yulab.utils

Suggests knitr, rmarkdown, prettydoc

VignetteBuilder knitr

ByteCompile true

License Artistic-2.0


BugReports https://github.com/GuangchuangYu/meshes/issues

biocViews Annotation, Clustering, MultipleComparison, Software

Encoding UTF-8

LazyData true

RoxygenNote 7.1.2

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enrichMeSH

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Author Guangchuang Yu [aut, cre], Erqiang Hu [ctb]
Maintainer Guangchuang Yu <guangchuangyu@gmail.com>

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Description

MeSH term enrichment analysis

Usage

```r
enrichMeSH(
  gene,
  MeSHDb,
  database = "gendoo",
  category = "C",
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe,
  qvalueCutoff = 0.2,
  minGSSize = 10,
  maxGSSize = 500,
  meshdbVersion = NULL
)
```

Arguments

gene a vector of entrez gene id
MeSHDb MeSHDb
database one of 'gendoo', 'gene2pubmed' or 'RBBH'
geneSim

pvalueCutoff Cutoff value of pvalue.
pAdjustMethod one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe background genes
qvalueCutoff qvalue cutoff
minGSSize minimal size of genes annotated by Ontology term for testing.
maxGSSize maximal size of genes annotated for testing
meshdbVersion version of MeSH.db. If NULL (the default), use the latest version.

Value
An enrichResult instance.

Author(s)
Guangchuang Yu

See Also
class?enrichResult

Examples
## Not run:
library(meshes)
library(AnnotationHub)
ah <- AnnotationHub()
qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
filepath_hsa <- qr_hsa[[1]]
db <- MeSHDbi::MeSHDb(filepath_hsa)
data(geneList, package="DOSE")
de <- names(geneList)[1:100]
x <- enrichMeSH(de, MeSHDb = db, database='gendoo', category = 'C')

## End(Not run)

geneSim

description
semantic similarity between two gene vector

Usage
geneSim(geneID1, geneID2 = NULL, measure = "Wang", combine = "BMA", semData)
Arguments

- geneID1: gene ID vector
- geneID2: gene ID vector
- measure: one of "Wang", "Resnik", "Rel", "Jiang" and "Lin"
- combine: One of "max", "avg", "rcmax", "BMA" methods, for combining semantic similarity scores of multiple DO terms associated with gene/protein.
- semData: gene annotation data for semantic measurement

Value

score matrix

Author(s)

Guangchuang Yu

Examples

```r
## library(meshes)
## library(AnnotationHub)
## ah <- AnnotationHub()
## qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
## filepath_hsa <- qr_hsa[[1]]
## db <- MeSHDbi::MeSHDb(filepath_hsa)
## hsamd <- meshdata(db, category="A", computeIC=T, database="gendoo")
data(hsamd)
geneSim("241", "251", semData=hsamd, measure="Wang", combine="BMA")
```

Description

Gene Set Enrichment Analysis of MeSH

Usage

```r
gseMeSH(
geneList, 
MeSHDb, 
database = "gendoo", 
category = "C", 
exponent = 1, 
minGSSize = 10, 
maxGSSize = 500, 
eps = 1e-10, 
pvalueCutoff = 0.05,
)```
pAdjustMethod = "BH",
verbose = TRUE,
seed = FALSE,
by = "fgsea",
meshdbVersion = NULL,
...
)

Arguments

geneList order ranked geneList
MeSHDb MeSHDb
database one of 'gendoo', 'gene2pubmed' or 'RBBH'
exponent weight of each step
minGSSize minimal size of each geneSet for analyzing
maxGSSize maximal size of genes annotated for testing
eps This parameter sets the boundary for calculating the p value.
pvalueCutoff pvalue Cutoff
pAdjustMethod pvalue adjustment method
verbose print message or not
seed logical
by one of 'fgsea' or 'DOSE'
meshdbVersion version of MeSH.db. If NULL (the default), use the latest version.
...
other parameter

Value
gseaResult object

Author(s)
Yu Guangchuang

Examples

## Not run:
library(meshes)
library(AnnotationHub)
ah <- AnnotationHub()
qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
filepath_hsa <- qr_hsa[[1]]

db <- MeSHDbi::MeSHDb(filepath_hsa)
data(geneList, package="DOSE")
y <- gseMeSH(geneList, MeSHDb = db, database = 'gene2pubmed', category = "G")

## End(Not run)
Description

construct annoData for semantic measurement

Usage

meshdata(MeSHDb = NULL, database, category, computeIC = FALSE)

Arguments

MeSHDb MeSHDb package
database one of supported database
category one of supported category
computeIC logical value

Value

a GOSemSimDATA object

Author(s)

Guangchuang Yu

Examples

## Not run:
library(meshes)
library(AnnotationHub)
ah <- AnnotationHub()
qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
filepath_hsa <- qr_hsa[[1]]
db <- MeSHDb::MeSHDb(filepath_hsa)
hsamd <- meshdata(db, category='A', computeIC=T, database="gendoo")
## End(Not run)
meshSim

Description

semantic similarity between two MeSH term vectors

Usage

meshSim(meshID1, meshID2, measure = "Wang", semData)

Arguments

- **meshID1**: MeSH term vector
- **meshID2**: MeSH term vector
- **measure**: one of "Wang", "Resnik", "Rel", "Jiang" and "Lin"
- **semData**: annotation data for semantic measurement, output by meshdata function

Value

score matrix

Author(s)

Guangchuang Yu [https://guangchuangyu.github.io](https://guangchuangyu.github.io)

Examples

```r
## library(meshes)
## library(AnnotationHub)
## ah <- AnnotationHub()
## qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
## filepath_hsa <- qr_hsa[[1]]
## db <- MeSHDbi::MeSHDb(filepath_hsa)
## hsamd <- meshdata(db, category='A', computeIC=T, database="gendoo")
## data(hsamd)
## meshSim("D000009", "D009130", semData=hsamd, measure="Resnik")
```

mesh_term_table

DATA Sets

Description

These datasets are used in meshes
reexports

Objects exported from other packages

Description

These objects are imported from other packages. Follow the links below to see their documentation.

DOSE  geneID, geneInCategory
enrichplot  cnetplot, dotplot, emapplot, gseaplot, heatplot, ridgeplot
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